

SEQUENCE LISTING

<110> Giesing, Michael

<120> Verfahren zum Untersuchen von Körperflüssigkeiten auf Krebszellen, dessen Verwendung, entsprechende Analysekits und Verwendung bestimmter Wirkstoffe zur Behandlung von Krebs

<130> M-43161-EP

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<151> 2002-08-20

<160> 22

<170> PatentIn version 3.1

<210> 1

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> forward primer (MNSOD)

<400> 1

gtcaccgagg agaagtacca gg

22

<210> 2

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse primer (MNSOD)

<400> 2

gggctgaggt ttgtccagaa

20

<210> 3

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> probe (MNSOD)

<400> 3

cgttggccaa gggagatgtt acagccc

27

<210> 4

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> forward primer (TXNRD1)

<400> 4

ggagggcaga cttcaaaagc tac

23

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<223> reverse primer (TXNRD1)

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acaaagtccca ggaccatcac ct

22

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<220>
<223> probe (TXNRD1)

<400> 6
ttgggctgcc tccttagcag ctgccca

26

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<220>
<223> forward primer (GPX1)

<400> 7
ctcggtttcc cgtgcaa

17

<210> 8
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<220>
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<400> 8
tgaagttggg ctcgaaccc

19

<210> 9
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> probe (GPX1)

<400> 9
agtttgggca tcaggagaac gccaaagaa

28

<210> 10

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<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer (GAPDH)

<400> 10
tgctgatgcc cccatgttc

19

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer (GAPDH)

<400> 11
ggcagtgtatgcatggactg

20

<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> probe (GAPDH)

<400> 12
tcaagatcat cagcaatgcc tcctgca

27

<210> 13
<211> 222
<212> PRT
<213> Homo sapiens

<400> 13

Met Leu Ser Arg Ala Val Cys Gly Thr Ser Arg Gln Leu Ala Pro Ala
1 5 10 15

Leu Gly Tyr Leu Gly Ser Arg Gln Lys His Ser Leu Pro Asp Leu Pro
20 25 30

Tyr Asp Tyr Gly Ala Leu Glu Pro His Ile Asn Ala Gln Ile Met Gln
35 40 45

Leu His His Ser Lys His His Ala Ala Tyr Val Asn Asn Leu Asn Val
50 55 60

Thr Glu Glu Lys Tyr Gln Glu Ala Leu Ala Lys Gly Asp Val Thr Ala
65 70 75 80

Gln Thr Ala Leu Gln Pro Ala Leu Lys Phe Asn Gly Gly His Ile

85

90

95

Asn His Ser Ile Phe Trp Thr Asn Leu Ser Pro Asn Gly Gly Gly Glu
 100 105 110

Pro Lys Gly Glu Leu Leu Glu Ala Ile Lys Arg Asp Phe Gly Ser Phe
 115 120 125

Asp Lys Phe Lys Glu Lys Leu Thr Ala Ala Ser Val Gly Val Gln Gly
 130 135 140

Ser Gly Trp Gly Trp Leu Gly Phe Asn Lys Glu Arg Gly His Leu Gln
 145 150 155 160

Ile Ala Ala Cys Pro Asn Gln Asp Pro Leu Gln Gly Thr Thr Gly Leu
 165 170 175

Ile Pro Leu Leu Gly Ile Asp Val Trp Glu His Ala Tyr Tyr Leu Gln
 180 185 190

Tyr Lys Asn Val Arg Pro Asp Tyr Leu Lys Ala Ile Trp Asn Val Ile
 195 200 205

Asn Trp Glu Asn Val Thr Glu Arg Tyr Met Ala Cys Lys Lys
 210 215 220

<210> 14
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<212> DNA
<213> Homo sapiens

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cagcagggcag ctggctccgg ctttgggtta tctgggttcc aggcagaagc acagcctccc	180
cgacctgccc tacgactacg gcgccttggg acctcacatc aacgcgcaga tcatgcagct	240
gcaccacagc aagcaccacg cggcctacgt gaacaacctg aacgtcaccc aggagaagta	300
ccaggaggcg ttggccaagg gagatgttac agcccagaca gctttcagc ctgcactgaa	360
gttcaatggt ggtggtcata tcaatcatag cattttctgg acaaacctca gccctaacgg	420
tggtggagaa cccaaagggg agttgcttgg agccatcaaa cgtgactttg gttcctttga	480
caagtttaag gagaagctga cggctgcata tgggggtgtc caaggctcag gttggggatt	540
gcttggtttc aataaggaac ggggacactt acaaattgct gcttgtccaa atcaggatcc	600
actgcaagga acaacaggcc ttattccact gctggggatt gatgtgtggg agcacgctta	660

ctacccatcg tataaaaatg tcaggcctga ttatctaaaa gctatttggaa atgtaatcaa	720
ctgggagaat gtaactgaaa gatacatggc ttgcaaaaag taaaccacga tcgttatgtct	780
gagtatgtta agctctttat gactgtttt gtatgttat agagtaactgc agaatacagt	840
aagctgctct attgttagcat ttcttgatgt tgcttagtca cttatccat aaacaactta	900
atgttctgaa taatttccta ctaaacattt tgttattggg caagtgattg aaaatagtaa	960
atgctttgtg tgattg	976

<210> 15
<211> 497
<212> PRT
<213> Homo sapiens

<400> 15

Met Asn Gly Pro Glu Asp Leu Pro Lys Ser Tyr Asp Tyr Asp Leu Ile				
1	5		10	15
	10	15		

Ile Ile Gly Gly Ser Gly Gly Leu Ala Ala Ala Lys Glu Ala Ala		
20	25	30

Gln Tyr Gly Lys Lys Val Met Val Leu Asp Phe Val Thr Pro Thr Pro		
35	40	45

Leu Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys		
50	55	60

Ile Pro Lys Lys Leu Met His Gln Ala Ala Leu Leu Gly Gln Ala Leu			
65	70	75	80

Gln Asp Ser Arg Asn Tyr Gly Trp Lys Val Glu Glu Thr Val Lys His		
85	90	95

Asp Trp Asp Arg Met Ile Glu Ala Val Gln Asn His Ile Gly Ser Leu		
100	105	110

Asn Trp Gly Tyr Arg Val Ala Leu Arg Glu Lys Lys Val Val Tyr Glu		
115	120	125

Asn Ala Tyr Gly Gln Phe Ile Gly Pro His Arg Ile Lys Ala Thr Asn		
130	135	140

Asn Lys Gly Lys Glu Lys Ile Tyr Ser Ala Glu Ser Phe Leu Ile Ala			
145	150	155	160

Thr Gly Glu Arg Pro Arg Tyr Leu Gly Ile Pro Gly Asp Lys Glu Tyr		
165	170	175

Cys Ile Ser Ser Asp Asp Leu Phe Ser Leu Pro Tyr Cys Pro Gly Lys
180 185 190

Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe
195 200 205

Leu Ala Gly Ile Gly Leu Gly Val Thr Val Met Val Arg Ser Ile Leu
210 215 220

Leu Arg Gly Phe Asp Gln Asp Met Ala Asn Lys Ile Gly Glu His Met
225 230 235 240

Glu Glu His Gly Ile Lys Phe Ile Arg Gln Phe Val Pro Ile Lys Val
245 250 255

Glu Gln Ile Glu Ala Gly Thr Pro Gly Arg Leu Arg Val Val Ala Gln
260 265 270

Ser Thr Asn Ser Glu Glu Ile Ile Glu Gly Glu Tyr Asn Thr Val Met
275 280 285

Leu Ala Ile Gly Arg Asp Ala Cys Thr Arg Lys Ile Gly Leu Glu Thr
290 295 300

Val Gly Val Lys Ile Asn Glu Lys Thr Gly Lys Ile Pro Val Thr Asp
305 310 315 320

Glu Glu Gln Thr Asn Val Pro Tyr Ile Tyr Ala Ile Gly Asp Ile Leu
325 330 335

Glu Asp Lys Val Glu Leu Thr Pro Val Ala Ile Gln Ala Gly Arg Leu
340 345 350

Leu Ala Gln Arg Leu Tyr Ala Gly Ser Thr Val Lys Cys Asp Tyr Glu
355 360 365

Asn Val Pro Thr Thr Val Phe Thr Pro Leu Glu Tyr Gly Ala Cys Gly
370 375 380

Leu Ser Glu Glu Lys Ala Val Glu Lys Phe Gly Glu Glu Asn Ile Glu
385 390 395 400

Val Tyr His Ser Tyr Phe Trp Pro Leu Glu Trp Thr Ile Pro Ser Arg
405 410 415

Asp Asn Asn Lys Cys Tyr Ala Lys Ile Ile Cys Asn Thr Lys Asp Asn
420 425 430

Glu Arg Val Val Gly Phe His Val Leu Gly Pro Asn Ala Gly Glu Val
 435 440 445

Thr Gln Gly Phe Ala Ala Ala Leu Lys Cys Gly Leu Thr Lys Lys Gln
 450 455 460

Leu Asp Ser Thr Ile Gly Ile His Pro Val Cys Ala Glu Val Phe Thr
 465 470 475 480

Thr Leu Ser Val Thr Lys Arg Ser Gly Ala Ser Ile Leu Gln Ala Gly
 485 490 495

Cys

<210> 16
 <211> 1314
 <212> DNA
 <213> Homo sapiens

<400> 16		
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cggcctgccg gcggggacga cagcattgcg cctgggtgca gcagtgtcg tctcgaaa	180	
ggaaagatat tttaaggcgt gtctgagcag acggggaggc tttccaaac ccaggcagct	240	
tctgtggcgtg tgcggtttcg acccggtcac acaaagcttc agcatgtcat gtgaggacgg	300	
tccggccctg aaaggaacgc tctcggaaatt ggccgcggaa accgatctgc ccgttgtt	360	
tgtgaaacag agaaagatac gcccgcattgg tccaacattt aaggcttatac aggagggcag	420	
acttcaaaac ctactaaaaa tgaacggccc tgaagatctt cccaaatcct atgactatga	480	
ccttatcatc attggaggtg gtcaggagg tctggcagct gctaaggagg cagccaaata	540	
tggcaagaag gtatggtcc tggactttgt cactccacc cctcttggaa ctagatgggg	600	
tcttggagga acatgtgtga atgtgggttg catacctaaa aaactgatgc atcaagcagc	660	
tttggtagga caagccctgc aagactctcg aaattatggaa tggaaagtgc aggagacagt	720	
taagcatgat tggacagaaa tgatagaagc tgtacagaat cacattggct ctttgaattt	780	
gggctaccga gtagctctgc gggagaaaaa agtcgtctat gagaatgctt atggcaatt	840	
tattggcct cacaggatta aggcaacaaa taataaaggc aaagaaaaaaa tttattcagc	900	
agagagttt ctcattgcca ctggtaaaag accacgttac ttggcatcc ctggtgacaa	960	
agaataactgc atcagcagtg atgatcttt ctccttgcct tactgccccg gtaagaccct	1020	
ggttgttggaa gcatcctatg tcgctttggaa gtgcgttggaa tttcttgcgt gtattggttt	1080	

aggcgtcaact gttatggtta ggtccattct tcttagagga tttgaccagg acatggccaa 1140
caaaaattggt gaacacatgg aagaacatgg catcaagttt ataagacagt tcgtaccaat 1200
taaagttgaa caaattgaag cagggacacc aggcccactc agagtagtag ctcagtcac 1260
caatagttag gaaatcattg aaggagaata taatacggtg atgctggcaa tagg 1314

<210> 17
<211> 201
<212> PRT
<213> Homo sapiens

<400> 17

Met Cys Ala Ala Arg Leu Ala Ala Ala Ala Gln Ser Val Tyr Ala
1 5 10 15

Phe Ser Ala Arg Pro Leu Ala Gly Gly Glu Pro Val Ser Leu Gly Ser
20 25 30

Leu Arg Gly Lys Val Leu Leu Ile Glu Asn Val Ala Ser Leu Cys Gly
35 40 45

Thr Thr Val Arg Asp Tyr Thr Gln Met Asn Glu Leu Gln Arg Arg Leu
50 55 60

Gly Pro Arg Gly Leu Val Val Leu Gly Phe Pro Cys Asn Gln Phe Gly
65 70 75 80

His Gln Glu Asn Ala Lys Asn Glu Glu Ile Leu Asn Ser Leu Lys Tyr
85 90 95

Val Arg Pro Gly Gly Phe Glu Pro Asn Phe Met Leu Phe Glu Lys
100 105 110

Cys Glu Val Asn Gly Ala Gly Ala His Pro Leu Phe Ala Phe Leu Arg
115 120 125

Glu Ala Leu Pro Ala Pro Ser Asp Asp Ala Thr Ala Leu Met Thr Asp
130 135 140

Pro Lys Leu Ile Thr Trp Ser Pro Val Cys Arg Asn Asp Val Ala Trp
145 150 155 160

Asn Phe Glu Lys Phe Leu Val Gly Pro Asp Gly Val Pro Leu Arg Arg
165 170 175

Tyr Ser Arg Arg Phe Gln Thr Ile Asp Ile Glu Pro Asp Ile Glu Ala
180 185 190

Leu Leu Ser Gln Gly Pro Ser Cys Ala
195 200

<210> 18
<211> 856
<212> DNA
<213> Homo sapiens

<400> 18
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cgccggcggc ggcccagtcg gtgtatgcct ttcggcgcg cccgttggcc ggccggggage 120
ctgtgagcct gggctccctg cggggcaagg tactacttat cgagaatgtg gcgtccctct 180
gaggcaccac ggtccgggac tacacccaga tgaacgagct gcagcggcgc ctggacccc 240
ggggccttgtt ggtgctcggc ttcccgtgca accagtttg gcattcaggag aacgccaaga 300
acgaagagat tctgaattcc ctcaagtacg tccggcctgg tggtggttgc gagcccaact 360
tcatgctctt cgagaagtgc gaggtgaacg gtgcgggggc gcaccctctc ttgccttcc 420
tgcgggaggc cctgccagct cccagcgaacg acgccaccgc gttatgacc gaccccaagc 480
tcatcacctg gtctccggtg tgtcgcaacg atgttccttg gaacttttag aagttcctgg 540
tgggcctgta cggtgtgccc ctacgcaggt acagccggcg cttccagacc attgacatcg 600
agcctgacat cgaagccctg ctgtctcaag ggcccagctg tgccctaggcc gcccctctt 660
ccccggctgc ttggcagttg cagtgtgttgc gtctcggggg gttttcatc tatgagggtg 720
tttcctctaa acctacgagg gaggaacacc ttgatcttac agaaaatacc acctcgagat 780
gggtgctggc cctgttgatc ccagtctctg ccagaccaag gcgagttcc ccactaataa 840
agtggccgggt gtcagc 856

<210> 19
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> probe (NMSOD)

<400> 19
gaacaacagg ccttattcca ctgctggggta ttgatgtgtg ggagcacgct tactaccttc 60

<210> 20
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> probe (TXNRD1)

<400> 20
cgtgttgcgg gctttcacgt actgggtcca aatgctggag aagttagacaca aggcttgca 60

<210> 21
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> probe (GPX2)

<400> 21
tacagccgca cttcccaac catcaacatt gagcctgaca tcaagcgct ccttaaagtt 60

<210> 22
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> probe (GPX3)

<400> 22
ctcttctggg aaccatgaa ggttcacgac atccgctgga actttgagaa gttcctgg 60